

EXHIBIT 3

CLUSTAL W (1.83): Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: G_kaustophilus 378 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 97
 Guide tree file created: [//ebi/extern/cluster-work/interactive/clusterw-20060731-05543637.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:6996
 Alignment Score 1906
 CLUSTAL-Alignment file created [//ebi/extern/clusterw-work/interactive/clusterw-20060731-05543637.aln]

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SEQ174 -----NSDIIIESFIPL 13
G_kaustophilus MNISIDREALAKSVQDVMAVSTRRTTIFILTGIKLTATASGVILTGSSEIS-IESFIPL 69
                      :*** *****

SEQ174 EKEGKLLVDVVRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRNLGN 73
G_kaustophilus EKEGKLLVDVVRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRNLGN 119
*****

SEQ174 ADEYFRLPQIEENVFQIPADLLKTVIRQTVFAVSTSETRPILTGUNVKVHSELVCTAT 133
G_kaustophilus ADEYFRLPQIEENVFQIPADLLKTVIRQTVFAVSTSETRPILTGUNVKVHSELVCTAT 179
*****

SEQ174 DSHRLAMRAVKKIESENEVSYNVPIPKSLNELSKIIILDDGNHFPVDIVMTANQVLFKAEN 193
G_kaustophilus DSHRLAMRAVKK-IESENEVSYNVPIPKSLNELSK-IIILDDGNHFPVDIVMTANQVLFKAEN 237
*****

SEQ174 LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTTLPG 253
G_kaustophilus LLFFSRLLDGNYPETARLIPTESKTTMIVNTKEFLQAI DRASLLAREGRNNVVKLTTLPG 297
*****

SEQ174 GMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMDALRALDGTDIQISFTGAMRP 313
G_kaustophilus GMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMDALRALDGTDIQISFTGAMRP 357
*****

SEQ174 FLLRPLHTOSMLQLILPVRTY 334
G_kaustophilus FLLRPLHTOSMLQLILPVRTY 378
*****

```

CLUSTAL W [1.83] Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ174 334 aa

Sequence 2: B_cereus 379 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 70

Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-05564381.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:6158

Alignment Score 1389

CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-05564381.aln]

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SEQ174 -----NSDISI-IESFIPLE 14
B_cereus MRFTIQKDYLVRSVQDVMKAVSSRTTIFILTGKIKVVATEEGVTLTGSDADISIESFIPVE 60
               **.******

SEQ174 KEGKLLVDVVKRPGSIVLOARFFSEIVKKLPQQTVEIETEDNFLTIIIRSGHSEFRINGLNA 74
B_cereus EDCKEIVEVKQSGSIVLQAKYFSEIVKKLPKETVEISVENHLMTKITSGKSEFNLGLDS 120
               :***:***:*****:*****:*****:***:***:***:*****:

SEQ174 DEYPRLPQIEEENVQIPADLLKTVIROTVFAVSTSETRFILTVGNWVKVHGLVCTATD 134
B_cereus ARYLPLPQIEEHHVFKLPDCLKHMIQTVFAVSTSETRFILTVGNWVKVYNELTCTIAD 180
               ***:*****:***:***:*****:*****:*****:***:***:***:

SEQ174 SHRLAMRKVKIIIESENEVSYNVVIPOKSLNELSKIIIDGDNHFDVMTANQVLFKAERL 194
B_cereus SHRLALRKAKIEGIADEFQANVVIPOKSLNELSK-ILDESEENVDIVITEYQVLFRTKHL 239
               *****:***:*****:*****:*****:*****:***:***:***:

SEQ174 LFFSRLLDGNYPETARLIPESKTTMIVNAKEFLQAIADRASLLAREGRNNVVKLTLPQG 254
B_cereus LFFSRLLDGNYPDTRLIPAESKTDIFVNTKEFLQAIADRASLLARDGRNNVVKLTLEQA 299
               *****:***:***:*****:*****:*****:*****:*****:

SEQ174 MLEISSISPEIGKVIEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISFTGAMRFF 314
B_cereus MLEISSNSPEIGKVVEEVQCEKVDGEELKISFSAKYMMDALKALDSTEIKISFTGAMRFF 359
               *****:***:***:*****:*****:*****:*****:*****:

SEQ174 LLRLFLTDSMLQLILEVPTY 334
B_cereus LLRTVNDESIIQLILEVPTY 379
               **:..:***:*****
    
```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: B_thuringiensis 379 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 70
 Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-06031038.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:6155
 Alignment Score 1367
 CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-06031038.aln]

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SEQ174 -----NSCISI-IIESFIPLE 14
B_thuringiensis MRFSIQKDYLVRSVQDVMKAVSSRTTIPILTGIKVVAEEGVTLTGSCADISIESFIPVE 60
                  ** * *****:

SEQ174 KEGKLLVDVKRFGSIVLQARFSEIVKKLPQQTVEIETEDNFLTIRSGHSEFRLNGLNA 74
B_thuringiensis EDGKEIVEVKQSGSIVLQARYFSEIVKKLPKETVELSVENHLMITKISGKSEFNGLDLS 120
                  :*: **::*****:*****:*****:*** * **::**::**::

SEQ174 DEYFRLPQIEENNVQIPADLLKTVIRQTVPFAVSTSETRPILTGVMWVKVEHGEVLVCATD 134
B_thuringiensis AEYFLLPQIEENHVEKIPDILLKHMIRQTVPFAVSTSETRPILTGVMWVKVYNSELTCIATD 160
                  *** *****:***:***:*****:*****:*****:***:***

SEQ174 SHRLAMRAVKIIESENEVSYNVPIPKSLNELSKIILDDGNHPVDIVMTANQVLFKAHL 194
B_thuringiensis SHRLALRAKAKIEGIVDEFQANVPIPKSLNELSK-ILDESEEMVDIVITEYQVLFRTKHL 239
                  *****:***:***:*****:*****:***:***:*****:***

SEQ174 LFFSRLLDGNYPETARLIFTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTLPGG 254
B_thuringiensis LFFSRLLLEGNYPDTRLIPAESKTDIFVNTKEFLQAI DRASLLARDGRNNVVKLTLEQA 299
                  *****:***:***:***:*****:*****:*****:***

SEQ174 MLEISSISPEIGKVTEQLQTESLEGEELNISFSKAKYMMDALRALDGDIDQISFTGAMRPF 314
B_thuringiensis MLEISSNSPEIGKVVEEVOCEKVDGEELKISFSKAKYMMDALKALDSTEIKISFTGAMRPF 359
                  *****:***:***:*****:*****:***:***:*****:***

SEQ174 LRLFLHTDSMLQLILPVRTY 334
B_thuringiensis LRTVNDESIQLILPVRTY 379
                  *:***:***:*****

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CLUSTAL W (1.55) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ174 334 aa

Sequence 2: B_weihenstephanensis 381 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned, Score: 69

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06054661.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:6123

Alignment Score 1374

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06054661.aln]

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SEQ174                      -----NSDISI-IESFIPLE 14
B_weihenstephanensis      MRFTIQKDYLVKRSVDVNVKAVSSRTTIPILTGKVVATEEGVTLTGSDADISIESFIPVE 60
                               .**.******.

SEQ174                      KEGKLLVDVKRPGSIVLQARFFSEIVKKLPQOTVEIETEDNFLTIRSGHSEFRLNGLNA 74
B_weihenstephanensis      DAGKEIVIEQSGSIIILQAKYFSEIVKKLPKETVEISVENHFMFKIKSGKSEFNGLNGLDA 120
                               .**.:*****.*****.*****.*****.*****.*****.*****.

SEQ174                      DEYFRLPQIEEENVFQIPADLLKTVINQTVFAVSTSETRPILTCVNVKVEHGEVLVCTATD 134
B_weihenstephanensis      AEYPLLPQIEEHVVFQIFDILLKHMIRQTVFAVSSSETRPILTCVNVKVVYNSLTCATD 180
                               ***.*****.:*****.*****.*****.*****.*****.*****.

SEQ174                      SHRLAMRKVKIIES--ENEVSYNVVIIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAE 192
B_weihenstephanensis      SHRLALRKAKIEGYNIADFPQANVVIIPGKSLSELK-ILDESEEMVDIVITEYQVLFRTK 239
                               *****.***.*****.:*****.*****.*****.*****.*****.

SEQ174                      HLLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAIADRASLLAREGRNNVVKLTLP 252
B_weihenstephanensis      HLLFFSRLLDGNYPDITRLIPAESKTDIEFVNTKEFLQAIADRASLLARDGRNNVVKLTLE 299
                               *****.:*****.*****.:*****.*****.*****.*****.

SEQ174                      GGMLEISSISFEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISFTGAMR 312
B_weihenstephanensis      GGMLEISSNAFEIGKVVEVQCENVGEEELKISFSAKYMMDALKALDSTEIKVFTGAMR 359
                               *****.:*****.:*****.:*****.:*****.:*****.:*****.

SEQ174                      PFLRLPLHTDSMLQLILPVRTY 334
B_weihenstephanensis      PFLIRTVNDDSIQLILPVRTY 381
                               ***.:**.******
    
```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: B_subtilis 378 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 69
 Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-06092781.dnd]
 Start of Multiple Alignment
 There are 2 groups
 Aligning...
 Group 1: Sequences: 2 Score: 6121
 Alignment Score 1379
 CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-06092781.aln]

```

SEQ174      -----NSDISIIIESFIPL 13
B_subtilis  MKFTIQKDLRVESVQDVLKAVSSRTTTPILTGIKIVASDDGVSTGSDSDIS-IESFIPIK 59
              :****
SEQ174      EKEGKLLVDVKKRPGSIVLQARFFSEIVKKLPQOTVEIETEDNFLTIIIRSGHSEFRNLGN 73
B_subtilis  EEGDKIEVITIEQPGSIVLQARFFSEIVKKLPMTATVEIVQNOYLTIIIRSGKAEFNLGLD 119
              *:.* :*****
SEQ174      ADEYPRLPQIEENVPQIPADLLKTVIRQTVFAVSTSETRPILTGVNWKVEGELVCTAT 133
B_subtilis  ADEYPHLPQIEEHAIQIPTDLLNLIRQTVFAVSTSETRPILTGVNWKVEQSEILCTAT 179
              *****:.*:****
SEQ174      DSHRLAMRKVKIIESENEVSYNVVIPIGKSLNELSKIILDDGNHPVDIVMTANQVLFKAEN 193
B_subtilis  DSHRLALRAKALDIFE-DRSYNVVIPIGKSLTELSK-IILDDNQELVDIVITETOVLFKARN 237
              *****:.* :*****
SEQ174      LLFESRLLDGNYPETARLIPTESKTTMIVNAKEFLQAIADRASLLAREGRNNVVKLTPLPG 253
B_subtilis  VLFESRLLDGNYPOTTSLIPQDSKTEIIVNTKEFLQAIADRASLLAREGRNNVVKLSAKPA 297
              :*****:.* :****
SEQ174      GMLIEISSISPEIGKVTEQLQTESLEGEELNISFSKAYMDALRALDGTDIQISFTGAMRF 313
B_subtilis  ESTEISSNSPEIGKVVEAIVADQIEGEELNISFSKAYMLDALKVLEGAEIRVSFTGAMRF 357
              :**** :.* :*****
SEQ174      FLRLPLHTDSMLQLILPVRTY 334
B_subtilis  FLIRTPNDEITVQLILPVRTY 378
              **:.* :*****
    
```

CLUSTAL W (1.83) multiple sequence alignment

Sequence format is Pearson

Sequence 1: SEQ174 334 aa

Sequence 2: B_licheniformis 378 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned, Score: 69

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06105976.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:6097

Alignment Score 1371

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06105976.aln]

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SEQ174                                     -----NSDSIIIESFIPL 13
B_licheniformis                          MKFTICKRLVESVQDVLKAVSSRTTIPILTGIRIVASDEGVSLTGSDDIS-IESFIPL 59
                                           :****
SEQ174                                     EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQOTVRIETEDNFTIIRSGHSEERLNCIN 73
B_licheniformis                          EDGDLIEIVTIEQPGSIVLQARFFSEIVKKLPMSVTEIEVQNOYLTIIISGKAEFNGLD 119
                                           ". . : * ::*****.*****.:::*****:..****:
SEQ174                                     ADEYPRLLPQIEEENVFQIADLLKTVIRQTVFAVSTSETRPILTGYNWKVEHGELVCTAT 133
B_licheniformis                          ASEYPLLPQIEEHAFQIPTDLLKNLIRQTVFAVSTSETRPILTGYNWNVTGELICTAT 179
                                           ".*** *****.:****:****:*****.*****.* ****:****
SEQ174                                     DSHRLAMKVKKIISENEVSNVVIIPGKSLNELSKIIIDDCGNHFVDIVMTANQVLFKAER 193
B_licheniformis                          DSHRLALRAKALDINE-DSSYNVVIIPGKSLTELSK-ILDDHQLVDIVITETQVLFKTRN 237
                                           *****:*. : * : *****.**** * * * : * * * : .*****:
SEQ174                                     LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTLPG 253
B_licheniformis                          VLFFSRLLDGNYPDTNRLIPQESKTNLI VNTKEFLQAI DRASLLAREGRNNVVKLSAAAN 297
                                           :*****:**** * * * :*****.*****:..
SEQ174                                     GMLEISSISPEICKVTEQLQTESLEGEELNISFSKAYMMDALRALDGTDIQISFTGAMRP 313
B_licheniformis                          ESIEISSNSPEIGKV/ETVNAEQIEGEDLKISFSKPYMLDAKVLGEDIHVSETGAMRP 357
                                           :**** *****. :*:****:****.***:***:.* *+:*****
SEQ174                                     FLIRPLMTDSMLQLILPVRTY 334
B_licheniformis                          FLIRTPNDDSI VQLILPVRTY 378
                                           **:*. : *+:*****

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